Claims

1. Labelled or unlabelled nucleic acid to specifically bind to the DNA of human adenoviruses (HAdV DNA), whereby the nucleic acid
   a) possesses the sequence SEQ ID NO. 1, SEQ ID NO. 2, or SEQ ID NO. 3,
   b) possesses a sequence with a homology greater than 78% with respect to SEQ ID NO. 1, SEQ ID NO. 2, or SEQ ID NO. 3, or
   c) is complementary with respect to a nucleic acid according to a) or b).

2. Method for the detection of HAdV DNA in a sample, comprising the following steps:
   - Providing a sample possibly containing HAdV DNA,
   - Providing a probe that can specifically bind to the DNA of at least 35 different HAdV serotypes,
   - Mixing the probe with the sample,
   - Amplification of regions of DNA of each of the 35 HAdV actually present in the sample, so that the section to which said probe can specifically bind will be amplified as well,
   - Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,
   - Detection of amplified DNA regions to which a probe has bound.

3. Method for the detection of HAdV DNA in a sample, comprising the following steps:
   - Providing a sample possibly containing HAdV DNA,
   - Providing at least one primer pair that can specifically bind to the DNA of at least 25 different HAdV serotypes,
   - Mixing the at least one primer pair with the sample,
   - Establishing conditions that allow one of the primers to specifically bind to one of the DNA strands of every single one of said 25 HAdV types,
   - Amplification of the regions – flanked by the at least one primer pair – of the DNA of each of the 25 HAdV serotypes actually present in the sample,
   - Detection of amplified DNA regions.

4. Method for the detection of HAdV DNA in a sample, comprising the following steps:
   - Providing a sample potentially containing HAdV DNA,
   - Providing at least one primer pair that can specifically bind to the DNA of at least 15 different HAdV serotypes,

- Providing a probe that can specifically bind – in the regions flanked by the at least one primer pair – to the DNA of the same at least 15 different HAdV serotypes,
- Mixing the at least one primer pair with the sample,
- Mixing the probe with the sample,
- Establishing conditions that allow one of the primers to anneal to one of the DNA strands of every single one of said 15 HAdV types,
- Amplification of the regions of the DNA – flanked by the at least one primer pair – of each of the 15 HAdV serotypes actually present in the sample,
- Establishing conditions that allow the probe to specifically bind to sections of the amplified regions,
- Detection of amplified DNA regions to which a probe has bound.

5. Method according to one of claims 2 to 4, characterized in that no degenerate primers are used in the amplification.

6. Method according to one of claims 2 to 5, characterized in that in the amplification one employs fewer than 11, preferably fewer than 5, and especially preferred fewer than 3 different primers.

7. Method according to one of claims 2 to 6, characterized in that nucleic acids according to claim 1 are used as primers in the amplification.

8. Method according to one of claims 2 to 7, characterized in that a nucleic acid according to claim 1 is used as probe.

9. Method according to one of claims 2 to 8, characterized in that the amplified region comprises ≤500 base pairs, preferably ≤300, and especially preferred ≤150 base pairs.

10. Method according to one of claims 2 to 9, characterized in that the detection of the amplified DNA regions is performed under real-time conditions (a) during and/or (b) after one, several, or each amplification step.

11. Method according to one of claims 2 to 10, characterized in that the detection of the amplified DNA regions is a quantitative detection.

12. Method according to one of claims 2 to 11, characterized in that as primers one uses nucleic acids, which in accordance with claim 1 are homologous with respect to the sequences SEQ ID NO. 1 and SEQ ID NO. 2, and/or as probe one uses a labelled nucleic acid that in accordance with claim 1 is homologous with respect to sequence SEQ ID NO. 3 or is complementary with respect to such a homologous sequence.

13. Method according to one of claims 2 to 12, characterized in that a TaqMan PCR process is used for amplification and detection.

14. Method according to one of claims 2 to 13, characterized in that the annealing in the amplification step takes place at ≥ 48 °C, preferred at ≥ 50 °C, more preferred at ≥ 53 °C, and even more preferred at ≥ 55 °C.

15. Kit, comprising a primer pair and a probe, each consisting of nucleic acids according to claim 1.

16. Use of one or several nucleic acids according to claim 1, or of a kit according to claim 15, in the detection of HAdV DNA.

17. Method for characterizing HAdV serotypes, comprising the following steps:
    - Detection of HAdV DNA in a sample in accordance with one of claims 2 to 14
    - Characterizing detected HAdV DNA present in the sample.